

SCORE Search Results Details for Application 10552515 and Search Result 20080624_083145_us-10-552-515-1.rag.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_083145_us-10-552-515-1.rag.

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 24, 2008, 08:32:16 ; Search time 263 Seconds
(without alignments)
2135.186 Million cell updates/sec

Title: US-10-552-515-1

Perfect score: 4950

Sequence: 1 MRMAATAWAGLQGPPLPTLC.....SELSSHWTPTVPKASQLQQ 933

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000:*

4: geneseqp2001:*

5: geneseqp2002:*

6: geneseqp2003a:*

7: geneseqp2003b:*

8: geneseqp2004a:*

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9:  geneseqp2004b:*
10:  geneseqp2005:*
11:  geneseqp2006:*
12:  geneseqp2007:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	4950	100.0	933	8	ADT77664	Adt77664 Splice va
2	4950	100.0	933	11	AEL84788	Ael84788 Tumor mar
3	4531.5	91.5	885	10	AEB13426	Aeb13426 Human pro
4	4364.5	88.2	843	10	AEB13424	Aeb13424 Human pro
5	3736	75.5	898	4	ABG15488	Abg15488 Novel hum
6	1531.5	30.9	920	6	ADB64420	Adb64420 Human pro
7	1511.5	30.5	920	6	ABP58666	Abp58666 Human dih
8	1504	30.4	981	8	ADK52114	Adk52114 Human ato
9	1504	30.4	981	12	AEN06206	Aen06206 Human eso
10	1489	30.1	1017	12	AFB77190	Afb77190 Mouse TM-
11	1488	30.1	960	11	AEG11142	Aeg11142 Human tra
12	1479.5	29.9	840	11	AEG11146	Aeg11146 Human tra
13	1464	29.6	1003	7	ADG48280	Adg48280 Human ret
14	1455	29.4	913	11	AEH82071	Aeh82071 Human gna
15	1445	29.2	1219	4	ABB62812	Abb62812 Drosophil
16	1445	29.2	1219	10	AFB95185	Afb95185 Fruit fly
17	1402.5	28.3	910	6	ADC42854	Adc42854 REMAP pro
18	1402.5	28.3	910	11	AEL84658	Ael84658 Tumor mar
19	1369.5	27.7	1075	4	ABB65993	Abb65993 Drosophil
20	1369.5	27.7	1075	10	AFC04729	Afc04729 Fruit fly
21	1367.5	27.6	712	11	AEG11145	Aeg11145 Human tra
22	1199.5	24.2	1058	4	ABB65022	Abb65022 Drosophil
23	1199.5	24.2	1058	10	AFC01816	Afc01816 Fruit fly
24	1154	23.3	596	6	ADB64387	Adb64387 Human pro
25	1061.5	21.4	594	4	AAB92637	Aab92637 Human pro
26	1061.5	21.4	594	5	ABP43811	Abp43811 FLJ10261
27	1061.5	21.4	594	8	ADJ75429	Adj75429 Marker ge
28	1061.5	21.4	594	8	ADN04848	Adn04848 Antipsori
29	1061.5	21.4	594	11	AEG11143	Aeg11143 Human FLJ
30	1037.5	21.0	782	6	ADX42387	Adx42387 Human col
31	1037.5	21.0	782	7	ADT95905	Adt95905 Colon can
32	1037.5	21.0	782	8	ADQ96288	Adq96288 T cell ac
33	1037.5	21.0	782	8	ADQ96104	Adq96104 T cell ac
34	912.5	18.4	475	6	ADB64962	Adb64962 Human pro
35	905	18.3	642	7	ADM05798	Adm05798 Human pro

36	905	18.3	642	10	AEC88728	Aec88728	Human	cDN
37	905	18.3	642	11	AEG11144	Aeg11144	Human	FLJ
38	819.5	16.6	443	5	ABP41785	Abp41785	Human	ova
39	817.5	16.5	179	6	AAO29613	Aao29613	Human	Nov
40	784.5	15.8	390	5	ABB90382	Abb90382	Human	pol
41	735	14.8	139	5	AAE24066	Aae24066	Human	pro
42	722.5	14.6	360	4	AAM40391	Aam40391	Human	pol
43	711.5	14.4	346	8	ADP29628	Adp29628	Human	sec
44	695.5	14.1	608	8	ADQ96298	Adq96298	T cell	ac
45	695.5	14.1	608	8	ADQ96286	Adq96286	T cell	ac

ALIGNMENTS

RESULT 1

ADT77664

ID ADT77664 standard; protein; 933 AA.

XX

AC ADT77664;

XX

DT 15-JUN-2007 (revised)

DT 13-JAN-2005 (first entry)

XX

DE Splice variant-novel gene expressed in prostate (SV-NGEP) polypeptide.

XX

KW Splice variant-novel gene expressed in prostate; SV-NGEP; human;

KW prostate cancer; cytostatic; gene therapy; immunotherapy; BOND_PC;

KW NGEP long variant; NGEP long variant [Homo sapiens]; GO5886.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .345

FT /label= Cytoplasmic

FT Region 157. .933

FT /note= "An immunogenic fragment comprising 8 consecutive amino acids that specifically binds to an antibody that specifically binds to a polypeptide comprising amino acids 157-933 is referred to in Claim 1"

FT Region 170. .178

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 215. .223

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 258. .266

FT /note= "Epitope, predicted to bind HLA2-01"

FT Domain 346. .368

FT /label= Transmembrane

FT Domain 369. .421

FT /label= External
FT /note= "Cell surface"
FT Region 403. .411
FT /note= "Epitope, predicted to bind HLA2-01"
FT Domain 422. .441
FT /label= Transmembrane
FT Region 427. .435
FT /note= "Epitope, predicted to bind HLA2-01"
FT Domain 442. .501
FT /label= Cytoplasmic
FT Domain 502. .524
FT /label= Transmembrane
FT Domain 525. .543
FT /label= External
FT /note= "Cell surface"
FT Domain 544. .566
FT /label= Transmembrane
FT Region 557. .565
FT /note= "Epitope, predicted to bind HLA2-01"
FT Region 562. .570
FT /note= "Epitope, predicted to bind HLA2-01"
FT Domain 567. .586
FT /label= Cytoplasmic
FT Domain 587. .609
FT /label= Transmembrane
FT Domain 610. .714
FT /label= External
FT /note= "Cell surface"
FT Domain 715. .737
FT /label= Transmembrane
FT Domain 738. .761
FT /label= Cytoplasmic
FT Domain 762. .784
FT /label= Transmembrane
FT Domain 785. .933
FT /label= External
FT /note= "Cell surface"
FT Region 846. .854
FT /note= "Epitope, predicted to bind HLA2-01"
XX
PN WO2004092213-A1.
XX
PD 28-OCT-2004.
XX
PF 05-APR-2004; 2004WO-US010588.
XX
PR 08-APR-2003; 2003US-0461399P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Pastan I, Bera TK, Lee B;XX
DR WPI; 2004-758338/74.
DR N-PSDB; ADT77665.
DR PC:NCBI; gi48093524.XX
PT New Splice Variant-Novel Gene Expressed in Prostate polypeptide or
PT encoding nucleic acid molecule for diagnosing, preventing or treating
PT cancer, especially prostate cancer.XX
PS Claim 1; SEQ ID NO 1; 88pp; English.XX
CC The present sequence is the protein sequence of splice variant-novel gene
CC expressed in prostate (SV-NGEP). SV-NGEP is identical to NGEP from amino
CC acid 1-157, diverging from amino acid 158. Expression analysis in 76
CC normal and foetal tissues showed SV-NGEP to be strongly expressed only in
CC a prostate sample. Claimed methods for detecting prostate cancer in a
CC subject comprise: contacting the sample with an antibody that
CC specifically binds a SV-NGEP polypeptide and detecting the formation of
CC an immune complex; or detecting an increase in expression of SV-NGEP
CC polypeptide or mRNA. Antibodies to an SV-NGEP polypeptide can be used to
CC detect metastatic prostate cancer cells at locations other than the
CC prostate. A claimed method for producing an immune response against a
CC cell expressing SV-NGEP, for example in a subject with prostate cancer,
CC comprises administering the polypeptide, or a polynucleotide encoding it,
CC to produce an immune response that decreases growth of the prostate
CC cancer. A claimed method for inhibiting the growth of a malignant cell
CC that expresses SV-NGEP comprises culturing cytotoxic T lymphocytes (CTLs)
CC with SV-NGEP to produce activated CTLs that recognise an NGEP expressing
CC cell, and contacting the malignant cell with the activated CTLs.
CC Alternatively, growth of a malignant cell is inhibited by contact with an
CC antibody that specifically binds an SV-NGEP polypeptide, where the
CC antibody is linked to an effector molecule (chemotherapeutic agent or
CC toxin) that inhibits growth of the malignant cell. This may be performed
CC in vivo. Kits for detecting an SV-NGEP polypeptide or polynucleotide in a
CC sample are also claimed.CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 4950; DB 8; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHARWAMTSETSSGSHCARSRMLRRRA 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAEWAMTSETSSGSHCARSRMLRRRA	60
Qy	61	QEEDSTVLIDVSPPEAEKRGSGYGSTAHASEPGGQQAACRAGSPAKPRIADFVLVWEEDL	120
Db	61	QEEDSTVLIDVSPPEAEKRGSGYGSTAHASEPGGQQAACRAGSPAKPRIADFVLVWEEDL	120
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASAWVLC	180
Db	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASAWVLC	180
Qy	181	YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVVDPVPEYYSCRFRVNLKPRF	240
Db	181	YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVVDPVPEYYSCRFRVNLKPRF	240
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Qy	301	PPEGPQAPRNLNQRQVLFQHWRWGKWNKYQPLDHVRRYFGEKVALYFAWLGFTGWLPA	360
Db	301	PPEGPQAPRNLNQRQVLFQHWRWGKWNKYQPLDHVRRYFGEKVALYFAWLGFTGWLPA	360
Qy	361	AVVGTFLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLSSACALAQAGRLFDH	420
Db	361	AVVGTFLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLSSACALAQAGRLFDH	420
Qy	421	GGTVFFSLFMALWAVLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	421	GGTVFFSLFMALWAVLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLAAW	540
Db	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLAAW	540
Qy	541	ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFY	600
Db	541	ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFY	600
Qy	601	SSPVYIAFFKGRFVGYPNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVS	660
Db	601	SSPVYIAFFKGRFVGYPNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVS	660
Qy	661	LIPKLKGWWQKFLRSKKRAGASAGASQGPWEDDYELVPCEGLFDDEYLEMVLQFGFVTI	720
Db	661	LIPKLKGWWQKFLRSKKRAGASAGASQGPWEDDYELVPCEGLFDDEYLEMVLQFGFVTI	720
Qy	721	FVAACPLAPLFLALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	721	FVAACPLAPLFLALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780

Qy 781 AFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRCTCRYRAFRDDDGHYS 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 781 AFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRCTCRYRAFRDDDGHYS 840

Qy 841 QTYWNLLAIRLAFVIVFEHVVFSGRLLVVDIPESVEIKVKREYYLAKQALAENEVL 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 QTYWNLLAIRLAFVIVFEHVVFSGRLLVVDIPESVEIKVKREYYLAKQALAENEVL 900

Qy 901 FGTNGTKDEQPKGSELSSHWTPTVPKASQLQQ 933
 ||||||||||||||||||||||||||||||||
 Db 901 FGTNGTKDEQPKGSELSSHWTPTVPKASQLQQ 933

RESULT 2

AEL84788

ID AEL84788 standard; protein; 933 AA.

XX

AC AEL84788;

XX

DT 18-OCT-2007 (revised)

DT 15-JUN-2007 (revised)

DT 28-DEC-2006 (first entry)

XX

DE Tumor marker gene NGEP SEQ ID NO 155.

XX

KW cytostatic; diagnosis; prognosis; tumor marker; gene expression;
 KW drug screening; cancer; neoplasm; NGEP; BOND_PC; NGEP long variant;
 KW G05886.

XX

OS Homo sapiens.

XX

PN WO2006110593-A2.

XX

PD 19-OCT-2006.

XX

PF 07-APR-2006; 2006WO-US013172.

XX

PR 07-APR-2005; 2005US-0669342P.

PR 11-OCT-2005; 2005US-0725982P.

XX

PA (MACR-) MACROGENICS INC.

XX

PI Von Haller PD, Schummer M, Meyer DW, Schubert LA, Tjoelker LW;

XX

DR WPI; 2006-814687/82.

DR N-PSDB; AEL84787.

DR REFSEQ; NP_001001891.

DR PC:NCBI; gi48093524.

XX

PT Detecting or diagnosing cancer in a subject comprises determining expression of at least one gene, and comparing level of expression to a control sample from a normal subject, where increased expression level indicates cancer.

XX

PS Claim 8; SEQ ID NO 155; 583pp; English.

XX

CC The invention describes a method of detecting or diagnosing cancer in a subject comprising determining the expression level of at least one gene, and comparing the level of expression to a corresponding control sample from a normal subject, where cancer is detected or diagnosed if there is an increase in the expression level of the gene relative to the expression in the control sample. Also described are: identifying a compound to be tested for its ability to prevent, treat, manage, or ameliorate cancer or its symptom; a compound identified by the method; treating cancer in a patient; treating a cancer in a subject that is fully or partially refractory to a first treatment in a patient; and a pharmaceutical composition comprising an amount of an antibody selected from anti-SLC12A2, anti-FLJ23375, anti-GRM5, anti-TAS2R1, anti-NRXN2, anti-C14orf160, anti-MGC 15668, anti-MGC33486, anti-TMEM16F, anti-FAT, anti-KIAA0195, anti-LRFN, anti-NFASC, anti-BAT2D1, anti-MGC2963, anti-KIAA0685, anti-EDG3, anti-GGTL3, anti-PLVAP, anti-FLJ31528, anti-FLJ90709, anti-VEZATIN, anti-TMPRSS9, anti-ATP13A5, anti-PKHD1L1, anti-C2orf18, anti-ANKRD22, anti-FAM62B, anti-LOC57168, anti-CDKALL1, anti-SLC39A3v1, anti-SLC39A3v2, anti-BAT5, anti-TM9SF4, anti-DC2, anti-VAPB, anti-XTP3TPB, anti-TACSTD2, anti-FNDC3A, anti-GK001, anti-OCIAD2, anti-PR01855, anti-C20orf3, anti-SDFR1, anti-FLJ20481, anti-LENG4, anti-FLJ12443, anti-ARP5 Long, anti-ARP5 Short, anti-TMD0645, anti-NGEP, anti-IL1RAP1, anti-PLXNB1, anti-ATP2B2, anti~FLJ11848, anti-ENTPD2, anti-PPM1H, anti-KRTKAP3, anti-KCNC3, anti-TM9SF1, anti-ULBP1, anti-C19orf26, anti-KIAA830, anti-KIAA1244, anti-KIAA1797, anti-MGC26856, anti-NETO2, anti-SUSD2, anti-FOLR2, anti-EMR2, ENTPD1, anti-ATP10B, anti-PTK7, anti-FLJ14681, anti-C20orf22, anti-FLJ14281, anti-FAM8A1, anti-TMED7, anti-C20orf108, anti-ATAD1, anti-GPR154, anti-C14orf27, anti-OSAP, anti-FAD104, anti-FLJ90492, anti-SLC27A3, anti-RON, anti-ATP13A1, anti-DKFZP564D166, anti-ESSPL, anti-EXTL3, anti-KAI1, anti-KIAA0960, anti-MTRNL, anti-SLC27A1, anti-GRIA, anti-OR4M1, anti-KIAA1679, or anti-UPK-1b antibody, and a pharmaceutical carrier. The methods are useful for detecting, diagnosing, and treating cancer, e.g. colon, lung, ovary, prostate, pancreas, or bladder cancer. This is the amino acid sequence of NGEP, altered levels of expression are useful in the diagnosis or prognosis of cancer.

CC

CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed information from BOND.

XX

SQ Sequence 933 AA;

Query Match 100.0%; Score 4950; DB 11; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMAATAWAGLQGPPPLPTLCPAVRTGLYCRDQAHAAERWAMTSETSSGSHCARSRMLRRRA 60
 |||||||
 Db 1 MRMAATAWAGLQGPPPLPTLCPAVRTGLYCRDQAHAAERWAMTSETSSGSHCARSRMLRRRA 60

Qy 61 QEEDSTVLIDVSPPEAEKRGSGYSTAHASEPQQQAAACRAGSPAKPRIADFVLVWEEDL 120
 |||||||
 Db 61 QEEDSTVLIDVSPPEAEKRGSGYSTAHASEPQQQAAACRAGSPAKPRIADFVLVWEEDL 120

Qy 121 KLDRQQDSAARDRTDMHRTWRETFLDLNRAAGLCVDQQDVQDGNTTVHYALLSASAWVLC 180
 |||||||
 Db 121 KLDRQQDSAARDRTDMHRTWRETFLDLNRAAGLCVDQQDVQDGNTTVHYALLSASAWVLC 180

Qy 181 YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVVVPDVPEYYSCRFRVNKLPRF 240
 |||||||
 Db 181 YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVVVPDVPEYYSCRFRVNKLPRF 240

Qy 241 LGSDNQDTFFTSTKRHQILFEILAKTPYGEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT 300
 |||||||
 Db 241 LGSDNQDTFFTSTKRHQILFEILAKTPYGEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT 300

Qy 301 PPEGPQAPRLNQRQVLFQHWRWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLPA 360
 |||||||
 Db 301 PPEGPQAPRLNQRQVLFQHWRWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLPA 360

Qy 361 AVVGTFLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLSSACALAQAGRLFH 420
 |||||||
 Db 361 AVVGTFLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLSSACALAQAGRLFH 420

Qy 421 GGTVFFSLFMALWAVLLEYWKRKSATLAYERWDCTSVDYEDTEERPRPQFAASAPMTAPNPI 480
 |||||||
 Db 421 GGTVFFSLFMALWAVLLEYWKRKSATLAYERWDCTSVDYEDTEERPRPQFAASAPMTAPNPI 480

Qy 481 TGEDEPYFFPERSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW 540
 |||||||
 Db 481 TGEDEPYFFPERSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW 540

Qy 541 ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTREWEHRTQTKFEDATLKVFIGQFVNFY 600
 |||||||
 Db 541 ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTREWEHRTQTKFEDATLKVFIGQFVNFY 600

Qy 601 SSPVYIAFFKGRFVGPGNYHTLFGVRNECAAGGCLIELAQELLVIMVGKQVINNMQE 660
 |||||||
 Db 601 SSPVYIAFFKGRFVGPGNYHTLFGVRNECAAGGCLIELAQELLVIMVGKQVINNMQE 660

Qy 661 LIPKLKGWWQKFLRSKKRAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI 720

Db	661	LIPKLKGWWQFRLRSKKRAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Qy	721	FVAACPLAPLFALLNNNWEIRLDARKFVCEYRRPVAERAQDIGINWFHILAGLTHLAVISN	780
Db	721	FVAACPLAPLFALLNNNWEIRLDARKFVCEYRRPVAERAQDIGINWFHILAGLTHLAVISN	780
Qy	781	AFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDGHYS	840
Db	781	AFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDGHYS	840
Qy	841	QTYWNLLAIRLAFLVIVFEHVVFSGRLLLPVDIPESSVEIKVKREYYLAKQALAENEVL	900
Db	841	QTYWNLLAIRLAFLVIVFEHVVFSGRLLLPVDIPESSVEIKVKREYYLAKQALAENEVL	900
Qy	901	FGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ	933
Db	901	FGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ	933

RESULT 3

AEB13426

ID AEB13426 standard; protein; 885 AA.

XX

AC AEB13426;

XX

DT 22-SEP-2005 (first entry)

XX

DE Human prostate specific polypeptide #2.

XX

KW Screening; diagnosis; drug delivery; prostate specific polypeptide; cancer; prostate tumor; cytostatic; neoplasm.

XX

OS Homo sapiens.

XX

PN WO2005062788-A2.

XX

PD 14-JUL-2005.

XX

PF 16-DEC-2004; 2004WO-US042406.

XX

PR 22-DEC-2003; 2003US-0531809P.

XX

PA (AVAL-) AVALON PHARM INC.

XX

PI Weigle B, Ebner R;

XX

DR WPI; 2005-497793/50.

DR N-PSDB; AEB13425.

XX

PT Novel isolated prostate specific polypeptide, useful for treating cancer, and identifying agent that modulates activity of cancer related gene.

XX

PS Claim 12; SEQ ID NO 5; 59pp; English.

XX

CC The invention relates to an isolated prostate specific polypeptide comprising one or more immunogenic fragments. The invention also relates to a method of identifying an agent that modulates the activity of a cancer related gene involving contacting a compound with a cell containing a gene under conditions promoting the expression of the gene, detecting a difference in expression of the gene relative to when the compound is not present and identifying an agent that modulates the activity of a cancer related gene, a method of identifying an anti-neoplastic agent involving contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene modulator using and determining a decrease in neoplastic activity after contacting, when compared to when the contacting does not occur, or administering an agent first identified to an animal exhibiting a cancer condition and detecting a decrease in cancerous condition, a method of determining the cancerous status of a cell involving determining an increase in the level of expression in a cell of a gene where an elevated expression relative to a known non-cancerous cell indicates a cancerous state or potentially cancerous state, an antibody that reacts with a prostate specific polypeptide, an immunoconjugate comprising the antibody and a cytotoxic agent, a method of treating cancer involving contacting a cancerous cell in vivo with an agent having activity against a prostate specific polypeptide and an immunogenic composition the prostate specific polypeptide. The prostate specific polypeptide is useful for identifying an agent that modulates the activity of a cancer related gene. The immunogenic composition is useful for treating cancer, preferably prostate cancer in an animal, e.g. human, which involves administering the immunogenic composition that is sufficient to elicit the production of cytotoxic T lymphocytes specific for the prostate specific polypeptide. The invention is useful for identifying anti-neoplastic agents. This sequence represents a human prostate specific polypeptide of the invention.

XX

SQ Sequence 885 AA;

Query Match 91.5%; Score 4531.5; DB 10; Length 885;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 855; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Qy

1 MRMAATAWAGLQGPPLPTLCAPVRTGLYCRDQAHRAEWAMTSETSSGSHCARSRMLRRRA 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

5 MRMAATAWAGLQGPPLPTLCAPVRTGLYCRDQAHRAEWAMTSETSSGSHCA--RMLRRRA 62

Qy

61 QEEDSTVLIDVSPPEAEKRGSGYGSTAHASEPGGQQAACRAGSPAKPRIADFVLVWEEDL 120

Db	63	QEEDSTVLIDVSPPEAKRGSGYSTAHASEPGQQAACRAGSPAKPRI-DFVLVWEEDL	121
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCSVQQDQVQDGNTTVHYALLSASAWAVLC	180
Db	122	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCSVQQDQVQDGNTTVHYALLSASAWAVLC	181
Qy	181	YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRF	240
Db	182	YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRF	241
Qy	241	LGSDNQDFTFTSTKRHQILFEILAKTPYGEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	242	LGSDNQDFTFTSTKRHQILFEILAKTPYGEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	301
Qy	301	PPEGPQAPRLNQRQVLFQHWRWGKWNKYQPLDHVRYYFGEKVALYFAWLGFTGWLPA	360
Db	302	PPEGPQAPRLNQRQVLFQHWRWGKWNKYQPLDHVRYYFGEKVALYFAWLGFTGWLPA	361
Qy	361	AVVGTLVFLVGCFLVFSIDPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFH	420
Db	362	AVVGTLVFLVGCFLVFSIDPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFH	421
Qy	421	GGTVFFSLFMAILWAVLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	422	GGTVFFSLFMAILWAVLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	481
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSRGNTLAAW	540
Db	482	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSRGNTLAAW	541
Qy	541	ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDATLKVFIQFVNFY	600
Db	542	ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDATLKVFIQFVNFY	601
Qy	601	SSPVYIAFFKGRFVGPGNYHTLFGVRNECAAGGLIELAQELLVIMVGKQVINNMQEVT	660
Db	602	SSPVYIAFFKGRFVGPGNYHTLFGVRNECAAGGLIELAQELLVIMVGKQVINNMQEVT	661
Qy	661	LIPKLKGWWQFRLRSKRRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	662	LIPKLKGWWQFRLRSKRRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	721
Qy	721	FVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGINWFHILAGLTHLAVISN	780
Db	722	FVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGINWFHILAGLTHLAVISN	781
Qy	781	AFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAHNRTCRYRAFRDDGHYS	840

Db 782 AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDGHYS 841
Qy 841 QTYWNLLAIRLAFLVIVFE 858
||| ||| ||| ||| ||| ||| |||
Db 842 QTYWNLLAIRLAFLVIVFE 859

RESULT 4

AEB13424

ID AEB13424 standard; protein; 843 AA.

XX

AC AEB13424;

XX

DT 22-SEP-2005 (first entry)

XX

DE Human prostate specific polypeptide #1.

XX

KW Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW cancer; prostate tumor; cytostatic; neoplasm.

XX

OS Homo sapiens.

XX

PN WO2005062788-A2.

XX

PD 14-JUL-2005.

XX

PF 16-DEC-2004; 2004WO-US042406.

XX

PR 22-DEC-2003; 2003US-0531809P.

XX

PA (AVAL-) AVALON PHARM INC.

XX

PI Weigle B, Ebner R;

XX

DR WPI; 2005-497793/50.

DR N-PSDB; AEB13423.

XX

PT Novel isolated prostate specific polypeptide, useful for treating cancer,
PT and identifying agent that modulates activity of cancer related gene.

XX

PS Claim 12; SEQ ID NO 3; 59pp; English.

XX

CC The invention relates to an isolated prostate specific polypeptide
CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the

CC activity of a cancer related gene, a method of identifying an anti-
 CC neoplastic agent involving contacting a cell exhibiting neoplastic
 CC activity with a compound first identified as a cancer related gene
 CC modulator using and determining a decrease in neoplastic activity after
 CC contacting, when compared to when the contacting does not occur, or
 CC administering an agent first identified to an animal exhibiting a cancer
 CC condition and detecting a decrease in cancerous condition, a method of
 CC determining the cancerous status of a cell involving determining an
 CC increase in the level of expression in a cell of a gene where an elevated
 CC expression relative to a known non-cancerous cell indicates a cancerous
 CC state or potentially cancerous state, an antibody that reacts with a
 CC prostate specific polypeptide, an immunoconjugate comprising the antibody
 CC and a cytotoxic agent, a method of treating cancer involving contacting a
 CC cancerous cell in vivo with an agent having activity against a prostate
 CC specific polypeptide and an immunogenic composition the prostate specific
 CC polypeptide. The prostate specific polypeptide is useful for identifying
 CC an agent that modulates the activity of a cancer related gene. The
 CC immunogenic composition is useful for treating cancer, preferably
 CC prostate cancer in an animal, e.g. human, which involves administering
 CC the immunogenic composition that is sufficient to elicit the production
 CC of cytotoxic T lymphocytes specific for the prostate specific
 CC polypeptide. The invention is useful for identifying anti-neoplastic
 CC agents. This sequence represents a human prostate specific polypeptide of
 CC the invention.

XX

SQ Sequence 843 AA;

Query Match 88.2%; Score 4364.5; DB 10; Length 843;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 824; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Qy	1	MRMAATAWAGLQGPPLPTLCAPVRTGLYCRDQAH	ERWAMTSETSSGSHCARSRMLRRRA	60	
Db	5	MRMAATAWAGLQGPPLPTLCAPVRTGLYCRDQAH	ERWAMTSETSSGSHCA--RMLRRRA	62	
Qy	61	QEDSTVLIDVSPPEAKRGSGYGSTAHASEP	GGQQAACRAGSPAKPRIADFV	LVWEEDL	120
Db	63	QEDSTVLIDVSPPEAKRGSGYGSTAHASEP	GGQQAACRAGSPAKPRI-DFV	LVWEEDL	121
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGL	CVDQQDVQDGNTTVHYALLSAS	AWVLC	180
Db	122	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGL	CVDQQDVQDGNTTVHYALLSAS	AWVLC	181
Qy	181	YYAEDLRLKLPQELPNQASNWSAGL	LAWLGIPNVILLEVVPDV	PPEYYSCRFRVNKLPRF	240
Db	182	YYAEDLRLKLPQELPNQASNWSAGL	LAWLGIPNVILLEVVPDV	PPEYYSCRFRVNKLPRF	241
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPY	GHEKKNLLGIHQLLAEGVLSA	FPLHDGPFKT	300

Db	242	LGSDNQDTFFTSTKRHQILFEILAKTPYGH EKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	301
Qy	301	PPEGPQAPRLNQRQVLQHWRWGKWNKYQPLD HVRRYFGEKVALYFAWLGFYTGWLPA	360
Db	302	PPEGPQAPRLNQRQVLQHWRWGKWNKYQPLD HVRRYFGEKVALYFAWLGFYTGWLPA	361
Qy	361	AVVGTFLVGCFLVFSDIPTQELCGSKDSFEMC PLCLDCPFWLSSACALAQAGRLFDH	420
Db	362	AVVGTFLVGCFLVFSDIPTQELCGSKDSFEMC PLCLDCPFWLSSACALAQAGRLFDH	421
Qy	421	GGTVFFSLFMALWAVLLEYWKRKSATLAYER WDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	422	GGTVFFSLFMALWAVLLEYWKRKSATLAYER WDCSDYEDTEERPRPQFAASAPMTAPNPI	481
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVM VAVVMCLVSIILYRAIMAIVVSRSGN TLLAAW	540
Db	482	TGEDEPYFPERSRARRMLAGSVVIVVM VAVVMCLVSIILYRAIMAIVVSRSGN TLLAAW	541
Qy	541	ASRIASLTGSVNVNLVFI LILSKIYVSLAHVLTRWEMHRTQTKF EDAFTLKVFIGQFVN FY	600
Db	542	ASRIASLTGSVNVNLVFI LILSKIYVSLAHVLTRWEMHRTQTKF EDAFTLKVFIGQFVN FY	601
Qy	601	SSPVYIAFFKGRFVG YPGNYHTLF GVRNECAAGGCL IELAQELLVIMVG KQVINNM QE	660
Db	602	SSPVYIAFFKGRFVG YPGNYHTLF GVRNECAAGGCL IELAQELLVIMVG KQVINNM QE	661
Qy	661	LIPKLKGWWQKFR LRSKKRAGASAG ASQGP WEDDYELV PCEGLF DEYLE MVLQ FGFVTI	720
Db	662	LIPKLKGWWQKFR LRSKKRAGASAG ASQGP WEDDYELV PCEGLF DEYLE MVLQ FGFVTI	721
Qy	721	FVAACPLA PLFALLNN WVEIRLD ARKFV CEYRR VAERA QDIGI WFH ILAGL THL AVISN	780
Db	722	FVAACPLA PLFALLNN WVEIRLD ARKFV CEYRR VAERA QDIGI WFH ILAGL THL AVISN	781
Qy	781	AFLLA FSSDFL PRA YYRW TRA HDLRG FLN FTL RAR APSS AAHN RTC	827
Db	782	AFLLA FSSDFL PRA YYRW TRA HDLRG FLN FTL RAR APSS AAHN RTC	828

RESULT 5

ABG15488

ID ABG15488 standard; protein; 898 AA.

XX

AC ABG15488;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #15479.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder

RW Food supplement
XX
QS Name signature

XX HOMO sapiens.

XX
DD 11 OCT 2001

RE 29 MAR 2001: 2001WO US008631

XX 30 MAR 2001; 2001INC 050000051
XX
XX 31 MAR 2000; 2000INC 00540217

PR 23-AUG-2000; 2000US-00649167

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT

DR WPI; 2001-639362/73.

DR N-PSDB; AAS79675.
XX

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX
PS Claim 20; SEQ ID NO 45847; 103pp; English

XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences

xx

SO Sequence 898 AA

Query Match 75.5%; Score 3736; DB 4; Length 898;
 Best Local Similarity 82.3%; Pred. No. 0;
 Matches 727; Conservative 4; Mismatches 16; Indels 136; Gaps 6;

1 MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAAER----- 37
 ||||||| ||||||| ||||||| ||||||| |||||
 1 MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAAERATDVVLLAPFCQPKTRSHGTCPP 60

38 -----W---AMTSETS-----SG 47
 | |:| | | |
 61 TERDPRGEGSTEYPGRVDGIQGWGTRALTGWTDRLLCQACQTLPPRHFLPGARGWLGG 120

48 SHCA-----RSRMLRRRAQEEDSTVLIDVSPPEAEKRGSGYGH 87
 | ||| : ||||||| ||||||| |||||||
 121 SPCAHGQESLPSQPSPILLRVESVKSMLRRRAQEEDSTVLIDVSPPEAEKRGSGYGH 180

88 ASEPGQQAAACRAGSPAKPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDN 147
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 181 ASEPGQQAAACRAGSPAKPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDN 240

148 LRAAGLCVDQQDQDGNTTVHYALLSASAWAVLCYYAEDLRLKPLQELPNQASNWSAGLL 207
 ||||||| ||||||| ||||||| ||||||| ||||||| : | :
 241 LRAAGLCVDQQDQDGNTTVHYALLSASAWAVLCYYAEDLRLKPLQDYPTRPPTGRPACC 300

208 AWLGIPNVLLEVVDPVPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP 267
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 301 AWLGIPNVLLEVVDPVPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP 360

268 YGHEKKNLNGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRNLNQRQVLFQHWRWGKWN 327
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 361 YGHEKKNLNGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRNLNQRQVLFQHWRWGKWN 420

328 KYQPLDHVRRYFGEKVALYFAWLGFTGWLPAAVGTLVFLVGCLVFSDIPTQELCGS 387
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 421 KYQPLDHVRRYFGEKVALYFAWLGFTGWLPAAVGTLVFLVGCLVFSDIPTQELCGS 480

388 KDSFEMCPLCLDCPFWLSSACALAO---AGRLFDHGGTVFFSLFMALWAVLLEYWKR 443
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 481 KDSFEMCPLCLDCPFWLSSACALAOQVREEAGRLFDHGGTVFFSLFMALWAVLLEYWKR 540

444 KSATLAYERWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFERSRARRMLAGSVV 503
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 541 KSATLAYERWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFERSRARRMLAGSVV 600

504 IVVMVAVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNVLFILLSKI 563
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db	601	IVVMVAVVMCLVSIILYRAIMAIIVVSRSNTLLAAWASRIASLTGSVNLVFILILSKI	660
Qy	564	YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTL	623
Db	661	YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTL	720
Qy	624	FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFLRSKKRAGA	683
Db	721	FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFLRSKKRAGA	780
Qy	684	SAGASQGPWEDDYELVPCEGLFDEYLEM-----	711
Db	781	SAGASQGPWEDDYELVPCEGLFDEYLEMAGFCPNACPELVEPEKARDQPEARSAG	840
Qy	712	-----VLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKF	747
Db	841	QDSRPEAVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKF	883

RESULT 6

ADB64420

ID ADB64420 standard; protein; 920 AA.

XX

AC ADB64420;

XX

DT 15-JUN-2007 (revised)

DT 04-DEC-2003 (first entry)

XX

DE Human protein encoded by clone FEBRA20031280.

XX

KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour; BOND_PC; transmembrane protein 16D; transmembrane protein 16D (eight membrane-spanning domains); transmembrane protein 16D [Homo sapiens]; TMEM16D; FLJ34221; FLJ34272; FLJ35277; MGC130026; unnamed protein product; unnamed protein product [Homo sapiens].

XX

OS Homo sapiens.

XX

PN EP1308459-A2.

XX

PD 07-MAY-2003.

XX

PF 28-MAR-2002; 2002EP-00007401.

XX

PR 05-NOV-2001; 2001JP-00379298.

PR 25-JAN-2002; 2002US-0350978P.

XX

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

DR WPI; 2003-450961/43.

DR N-PSDB; ADB62450.

DR PC:NCBI; gi30520318.

XX

PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.

XX

PS Claim 1; Page; 222pp; English.

XX

CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 920 AA;

Query Match 30.9%; Score 1531.5; DB 6; Length 920;

Db 634 PLIQNWTR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTI 690
 Qy 721 FVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN 780
 |||| ||||| ||||| :|||||| ||| ::|||:||| :|||:|||||:||| :|:|||:
 Db 691 FVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWIYGILEGIGILSVITN 750
 Qy 781 AFLLAFLSSDFLPRAYYRW-----TRAHDLRGFLNFTLA-----RAP 816
 ||::| :|||:||| | : :|::| :|:
 Db 751 AFVIAITSDFIPRLVYAKYGPCAGQGEAQKCMVGYVNASLSVFRISDFENRSEPESDG 810
 Qy 817 SSFAAAHNRCTCRYRAFRDDDGH----YSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLL 871
 | |: :| ||| :||| | :| :|||:|||:|||:||| :|: |
 Db 811 SEFSGTPPLKYCRYRDYRDPHSHSLVPYGYTLQFWHVLALARLAFIIVFEHLVFCIKHLISYL 870
 Qy 872 VPDIPIESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHW 920
 :||:| :| :||| ||| :| :| :|:| :| :| :|:
 Db 871 IPDLPKDLRDRMRREKYLIQEMMYEAEELRLQKERKERKKNGKAHHNEW 919

RESULT 7

ABP58666

ID ABP58666 standard; protein; 920 AA.

XX

AC ABP58666;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human dihydropyrimidinase related protein 1-101.20.

XX

KW Human; dihydropyrimidinase related protein 1-101.20;

KW recombinant production; gene therapy; psychosis; development disorder;

KW uracil-related metabolic disorder; thymine-related metabolic disorder;

KW pyrimidine metabolic disorder.

XX

OS Homo sapiens.

XX

PN CN1364894-A.

XX

PD 21-AUG-2002.

XX

PF 10-JAN-2001; 2001CN-00105195.

XX

PR 10-JAN-2001; 2001CN-00105195.

XX

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2003-000532/01.

DB N-PSDB: ABZ57080

YY

PT New polypeptide-human dihydropyrimidinase relative protein 1-101, 20 and
PT polynucleotide for encoding such polypeptide.

xx

PS Claim 1; Page 28-30 (Disclosure); 36pp; Chinese

xx

CC The invention relates to human dihydropyrimidinase related protein 1-
CC 101.20 (ABP58666) and nucleic acids encoding it (ABZ57080). The protein
CC has a molecular weight of 101.2 kD. The invention also relates to a
CC method for the recombinant production of the protein, an antagonist of
CC the protein, and the use of the protein, gene and antagonist in
CC therapeutic applications. Dihydropyrimidinase related protein 1-101.20
CC can be used in the treatment of a variety of diseases such as psychosis,
CC development disorders and uracil- and thymine-related metabolic
CC disorders. The present sequence represents human dihydropyrimidinase
CC related protein 1-101.20

xx

SO Sequence 920 AA

Query Match 30.5%; Score 1511.5; DB 6; Length 920;
Best Local Similarity 37.6%; Pred. No. 1.2e-145;
Matches 357; Conservative 169; Mismatches 318; Indels 105; Gaps 29;

QY 44 TSSGSHCARSRMLRRRAQEEDSTVLID---VSPPEAE----KRGSYGST---AHASEP 91
 :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
 Ph 45 SSSCITNCITKTCVHVDVKA KPNVNLLEDELENVSGECKPDDSLIUGCNGNTSTSDPDKL 61

Qy 92 GGQQAAACRAGS----PAKPRIADFVLWEEDLKLDRQQDSAARDRTDMHRTWRETFLD 146
||: ; : | : | : ; : ; : | : ; : | : | : |

62 GGETVPERNKSNGLYFRDGKCRD-DYIIVYRK-----SNPOTEK----REVEER 105

Qy 147 NLRAAGLCVDQQDVQDGNTTVHYALLSASAWVLCKYYAEDLRLKLPQE---LPNQASNW 202

Db 106 NIRAEGLQMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYLYLPRRYKFM 164

Db 165 SRIDKQISRFRRWLPKPMRLDKETLPDLEENDCYTAPFSQQRHHFI-IHNKETFFNNA 223

Qy 254 KRHQILFEILAKTPYGHKEKNNLLGIHQQLAAFGVLSAAFPLHDGPFKTPPEGPQAPRLNQR 313
| :| : || : | | || :| ::|| | ||||||| :| ::| | |

224 TRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEEAAFPLHEGSYRSRKSNSIRTHGAENHR 282

DD 263 HLLIECWASWGVWIKIQLPDLVRRYIFGERKIGLYFAWLGWITGMELFPAAF1GLFVF1IGV1 342

374 LEVSDTPTQELCGSKDSFEMCPLC-LDCPFWLESSACALAQAGRLFDHGGTVFESLFLMAL 452

Db	343	TLDHSQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFNDNGATVFFAVFMAV	401
Qy	433	WA VLLLEYWKRKSATI LAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER	491
Db	402	WATVFLFWKRRRAVIA YDWLDWEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFT	461
Qy	492	SRARRMLAGSVVIVVMVAVVVMCLVSI LYL RAIMAIVVSRSGNTLLA-AWA----SRIA	545
Db	462	DKCSRLIVSASGIGFMICVVIAAVFGIVIYRVVTV-----STFAAFKWALIRNNSQVA	514
Qy	546	SLTGSVV--NLVFILILSKIYVSLAHVLT RWEMHRTQTKFEDA TLKVFIFQFVN FYSSP	603
Db	515	T-TGTAVCINF CIIMLLNVLYEKV ALLTNLEQPRTESEWENSFTLKMFLFQFVN LNSST	573
Qy	604	VYIAFFKG RFGVGP GNYHTLFG-VRNEECAAGGCLIELA QELLVIMVGKQVINNMQEVL	662
Db	574	FYIAFFLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCM QMGII MVLKQTWNNF MELGY	633
Qy	663	PKLKGWWQKFRRLRSKKR KAGASAGASQGPWEDDYELVPC E--GLFDEYLEMVLQFGFVTI	720
Db	634	PLIQNW WTR--RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLYDEYLEMILQFGFTT	690
Qy	721	FVAACPLAPL F ALLNNWVEIRLDARKFVCEYRRPVAERAQD IGFHILAGLTHLAVISN	780
Db	691	FVA AFPLAPL ALLNNIIEIRLDAYKEV TQWRRPLASRAK DIGIGY GILEGIGILSVITN	750
Qy	781	AFLLA FSSDFL P RAYYRW-----TRAHDLRGFLNFTLA-----RAP	816
Db	751	AFVIAITSDFIPR L VYAYK YGPCAGQGEAGQKCMVG YVNASLSVFRISDFENRSE PESDG	810
Qy	817	SSFAAAHN RCTCRYRAFRDDDG----YSQTYWNLLAIRLAFVIVF EHVVF SVGRLL DLL	871
Db	811	SEFGTPLK YCRYRDYRDPHSLVPYGYTLQFWHVL AARLAFIIVF EHLVFCIKHLIS YL	870
Qy	872	VPDIPESVEIKV KREYYLAQ QALAE NEVLF GFTNGTKD EOPKGSELSSHW	920
Db	871	IPDLPKDLRDRMRRE KYL IQEMM YEAELERLQKERKER KNGKAHHNEW	919

RESULT 8

ADK52114

ID ADK52114 standard; protein; 981 AA.

XX

AC ADK52114;

XX

DT 15-JUN-2007 (revised)

DT 20-MAY-2004 (first entry)

XX

DE Human atopic dermatitis/psoriasis-associated protein #29.
XX
KW Human; atopic dermatitis; psoriasis; dermatological; anti-inflammatory;
KW antipsoriatic; rash; BOND_PC; transmembrane protein 16C;
KW chromosome 11 open reading frame 25;
KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
KW transmembrane protein 16C (eight membrane-spanning domains);
KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
KW GO16021; GO4185; GO7001.
XX
OS Homo sapiens.
XX
PN WO2004016785-A1.
XX
PD 26-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-JP009999.
XX
PR 06-AUG-2002; 2002JP-00229319.
PR 14-MAY-2003; 2003JP-00136544.
XX
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
XX
PI Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
PI Mitsuishi K;
XX
DR WPI; 2004-214514/20.
DR N-PSDB; ADK52028.
DR PC:NCBI; gi13899227.
DR PC:SWISSPROT; Q9BYT9.
XX
PT Detecting atopic dermatitis or psoriasis comprises assaying levels of
PT expression of an indicator gene at a rash site and non-rash site of a
PT person with atopic dermatitis or psoriasis.
XX
PS Example 2; SEQ ID NO 147; 484pp; Japanese.
XX
CC The invention relates to detecting atopic dermatitis or psoriasis
CC comprising assaying the levels of expression of an indicator gene at a
CC rash site and non-rash site of a person with atopic dermatitis or
CC psoriasis, comparing these levels with those of a healthy person, and
CC determining that if the levels of indicators are higher or lower, then
CC this indicates the disease. Also included are a reagent for detecting
CC atopic dermatitis or psoriasis, a kit for screening for treatments, a
CC transgenic non human vertebrate animal models for the diseases, an agent
CC for inducing the diseases in mice and a DNA chip for assaying for the
CC indicator genes. The method is used for treatment, detection and animal
CC models for research of atopic dermatitis and psoriasis. The present

CC sequence is a protein encoded by an indicator gene of the invention.
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 981 AA;

Query Match 30.4%; Score 1504; DB 8; Length 981;
 Best Local Similarity 39.4%; Pred. No. 8.1e-145;
 Matches 329; Conservative 163; Mismatches 268; Indels 76; Gaps 24;

Qy 106 KPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNT 165
 | || |::|: :|::|: | || ||| |::|: :|:
 Db 161 KRRI-DYILVYR-----KTNIPYDKRNTFEKNLRAEGLMLEKEPA-IASP 203

Qy 166 TVHYALLSASAWVLCYAAEDLRLKLPLQ-----ELPNQASNWSAGLLAHLGIPNV 215
 : : | | || |::|: | : : : : | : :|:
 Db 204 DIMFIKIHIPWDTLCKYAERLNIRMPFRKKCYYTDGRSKSMGRMQTYFRIKDWMAQNPM 263

Qy 216 LLE--VVPDV-PPEYYSCRFRVNKLPRFLGSNDQDTFFTSTKRHQILFEILAKTPY--GH 270
 :|: |::|: |::|: |::|: |::|: |::|: |::|:
 Db 264 VLDKSAFPDLEESDCYTPGFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGI 322

Qy 271 EKKNLLGIHQLLAEGVLSAASFPLHDGPFK---PPEGPQAPRLNQRQVLFQHWRWGK 326
 | :|: |::|: | | ||| |::|: | :|:
 Db 323 SK---VGIRKLINNGSYIAAFPPHEGAYKSSQPIKTHGPQ---NNRHLLYERWARWGMW 375

Qy 327 NKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSIPTQELCG 386
 |:|:|: | |::|: | |::|: | |::|: | |::|:
 Db 376 YKHQPLDLIRLYFGEKIGLYFAWLGYTGMLIPAAIVGLCVFFYGLFTMNNSQVSQEICK 435

Qy 387 SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFSLFMALWAVLLEWKRS 445
 : : | |::|: | : | : | |::|: | |::|: | |::|:
 Db 436 ATEVF-MCPLCDKNCNSLQRLNDSCIYAKVTYLFDNGGTVFIAFMAIWATVLFWKRRR 494

Qy 446 ATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVI 504
 : | | | :|: | | | | | | | | | | | | | | |:
 Db 495 SILTYTWDLIEEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSDKVTRLVSVSGI 554

Qy 505 VVMVAVVMCLVSIILYR-AIMAIVVSRSGNLTLLAAWASRIASLTGSV-VNLVFILILSK 562
 |::|: | : |::|: | : | | | | | | | | | | |:
 Db 555 FFMISLVTAVFGVVVYRLVVMEQASFKNFIKQYW--QFATSAAVCINFIIIMLLNL 612

Qy 563 IYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNFYSSPVYIAFFKGRFVGYPGNYH 622
 | |::|: | | |::|: | | |::|: | | | | | | | |:
 Db 613 AYEKIAYLLTNLEYPRTESEWENSFALKMFLQFVNLNSSIFYIAFFLGRFVGHPGKYNK 672

Qy 623 LFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKLGWWQKFRRLRSKKRKA 681
 | | | | | | | | | | | | | | | | | | | | | | |:

Db	673	LFDRWRLEECHPSGCLIDLCLQMGVIMFLKQIWNNTMELGYPLIQNWWSRHKI-----KR	727
Qy	682	GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFTTIFVAACPLAPLFALLNNWVE	739
Db	728	GIH-DASIPQWENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAPFLAPLLALLNNIE	786
Qy	740	IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFASSDFLPRAYYRW-	798
Db	787	IRLDAYKFVTQWRRPLPARATDIGIWLGLGIGILAVITNAFVIAITSYDIPRFVYEYK	846
Qy	799	-----TRAHDLRGFLNFTLARAP-SSFAAAHNRTCRYRAFR-----DDDGHYSQTY	843
Db	847	YGPCANHVEPSENCLKGIVNNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQY	906
Qy	844	WNLLAIRLAFVIVFEHVVFSGRLLDLPDIPESEVIEKVKREYYLAKQALAENEV	899
Db	907	WHILAARLAFIIVFEHLVFGIKSFIAYLIPDVPKGLHDRIRREKYLVQEMMYEAL	962

RESULT 9

AEN06206

ID AEN06206 standard; protein; 981 AA.

XX

AC AEN06206;

XX

DT 15-JUN-2007 (revised)

DT 22-FEB-2007 (first entry)

XX

DE Human esophageal cancer-associated protein SEQ ID NO 231.

XX

KW diagnostic; metastasis; esophagus tumor; gastrointestinal disease;
 KW neoplasm; cytostatic; cancer; AXL; ZBTB11; TNFRSF14; NSUN5; SPEN; LTBP3;
 KW SYNGR1; SLC13A1; MAP3K12; GLYAT; ZNF659; B4GALT2; POGK; AQP3; CAPG;
 KW SLIT2; BOND_PC; transmembrane protein 16C;
 KW chromosome 11 open reading frame 25;
 KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
 KW transmembrane protein 16C (eight membrane-spanning domains);
 KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
 KW GO16021; GO4185; GO7001.

XX

OS Homo sapiens.

XX

PN WO2006118308-A1.

XX

PD 09-NOV-2006.

XX

PF 02-MAY-2006; 2006WO-JP309177.

XX

PR 02-MAY-2005; 2005JP-00134530.

PR 13-SEP-2005: 2005TP-00265645

PB 13-SEP-2005: 2005-TP-00265678

xx

PA (TOBA) TOBAY IND INC

PA (KYOU) UNIV KYOTO

vv

PI Akiyama H, Kozono S, Myomoto A, Nomura O, Nobumasa H, Tanaka Y;
PI Tomoda S, Shimada Y, Tsujiimoto G;

yy

DB WBT: 2007-110304/11

DB PC:NCBI: gi13899227

DB BC:SWISSRROT: 09BYT9

vv

PT Composition for determining occurrence/metastasis of esophageal cancer in subject, comprises an antibody binding to a polypeptide encoded by a polynucleotide having a sequence of genes e.g. AXL, ZBTB11 and TNFRSF14, and/or polynucleotides.

xx

PS Claim 1: SEQ ID NO 231: 142pp: Japanese

xx

CC This invention describes a novel composition for detecting metastasis of
CC esophageal cancer in a test subject. The composition contains a probe
CC derived from polynucleotides AXL, ZBTB11, TNFRSF14, NSUN5, SPEN, LTBP3,
CC SYNGR1, SLC13A1, MAP3K12, GLYAT, ZNF659, B4GALT2, POGK, AQP3, CAPG,
CC SLIT2, their variants or fragments and an antibody. The invention also
CC claims: a) a kit for detecting, determining or presuming the occurrence
CC or metastasis of esophageal cancer in a test subject; b) a DNA chip for
CC detecting, determining or presuming the occurrence or metastasis of
CC esophageal cancer and c) a method to detect, determine or presume the
CC occurrence or metastasis of esophageal cancer in a test subject by
CC detecting the presence of or amount or expression level of one or more
CC esophagus-cancer related target nucleic acid in a biological sample. The
CC method enables the rapid and convenient detection of occurrence or
CC metastasis of esophageal cancer in test subject with high sensitivity.
CC This sequence represents a protein used in the method of the invention

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

xx

SO Sequence 981 AA

Query Match 30.4%; Score 1504; DB 12; Length 981;
Best Local Similarity 39.4%; Pred. No. 8.1e-145;
Matches 329; Conservative 163; Mismatches 268; Indels 76; Gaps 24;

Ov

106 KPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCSVDDQVQDGNT 165

Ph

161 KBRI-DYLVYR-----KTNIPYDKBNTEEKNLRAEGLMLEKEPA-IASP 203

Qy	166	TVHYALLSASWA VLCYAAEDLRLKLPLQ-----ELPNQASNWSAGLLA WL GIPNV	215
	: : : :: : : : : : : : :		
Db	204	DIMFIKIHIPWDTLCKYAERLNIRMPFRKCYYT DGRSKSMGRMQTYFRRIKDWMAQNP	263
Qy	216	LLE--VVPDV-PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GH	270
	: : : : : : : : : : :		
Db	264	VLDKSAFPDLEESDCTGPF SRARIHHFI- INNKDTFFSNATRSRIVYHMLERTKYENGI	322
Qy	271	EKKNLLGIHQLLAEGVLSA A FP LHDGP FK---PPEGPQAPRLNQRQVLFQHWARWGK	326
	: : : : :		
Db	323	SK--VGIRKLINNGSYIAAFPPHEGAYKSSQPIKTHGPQ---NNRHLLYERWARWGMW	375
Qy	327	NKYQPLDHVRRYFGEKVALYFAWLGFYTGWL PAAVGT LVFLVGCF LVFS DIPTQELCG	386
	: : : : : :		
Db	376	YKHQPLDLIRLYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNNSQVSQEICK	435
Qy	387	SKDSFEMCPLC-LDCPFWLLSSACALAQA GRLFDHGGTVFFSLFMA LWAVL L EY WKRKS	445
	: : : : : : : :		
Db	436	ATEVF-MCPLCDKNC SLQRLNDSCIYAKV TYLF DNGGTVFFAIFMAI WATV FLE FWKRR	494
Qy	446	ATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPN P ITGEDEPYF PERSRARRMLAGSVVI	504
	: : : : : :		
Db	495	SILTYTWDLIEWEEEETLRPQFEAKYYKMEIVN P ITGKPEPHQPS DKVTRLLVSVSGI	554
Qy	505	VVMVAVVVMCLVSIILYR- AIMAIVVSRSGNTLLA AWA SRIASLTGSV- VNLV F IL LSK	562
	: : : : : : : : :		
Db	555	FFMISL VITAVFGVVVYRLVVM EQFASFKWNFIKQYW- QFAT SAAVCINFIIIMLLNL	612
Qy	563	IYVSLAHVLTRWEMHRTQKFEDAFTLKVFIFQFVN FYSSPVYIAFFKGRFVGYPGNYHT	622
	: : : :		
Db	613	AYEKIAYLLTNLEYPRTESEWENS FALKMFLQFVN L NSSIFYIAFFLGRFVGHPGKYNK	672
Qy	623	LFG-VRNEECAAGGCLIELA QELL VIMVGKQV INNMQM E V LIPKLKGW WQKFRLRSK RKA	681
	: :		
Db	673	LFDRWR LEECHPSGCLIDLCLQMGVIMFLQ IWN NFMELGYPLI QN WWSRH KI----KR	727
Qy	682	GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFTIFV AACPLA PLFALLNNWVE	739
	:		
Db	728	GIH-DASIPQWENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLA PL L ALLNNIIE	786
Qy	740	IRLDARKFVCEYRRPVAERAQD IGIWFH ILAGLTHAVISNAFLA FSSDFLPRAYYR-	798
	: :		
Db	787	IRLDAYKFVTQWRRPLPARATDIGIWL GILEGIGI LAVITNAF VIAITS D YIPRFVY EYK	846
Qy	799	-----TRAHDLRGFLNFTLARAP-SSFAAAHN RCTRYRAFR-----DDGHYSQTY	843
	: : : : : : : : : : :		
Db	847	YGPCANHVEPSENCLKG YVNNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQY	906
Qy	844	WNLLAIRLAFVIVFEHVVF SVGRLL L VPDIPESVEIKVKREYYLAKQALAENEV	899

|:::| ||||:||||:|| : : |::|: : ::|| || :: : | |:
Db 907 WHILAARLAFIVFEHLVFGIKSFIAYLIPDVPKGLHDRIRREKYLVQEMMYEAL 962

RESULT 10

AFB77190

ID AFB77190 standard; protein; 1017 AA.

XX

AC AFB77190;

XX

DT 28-JUN-2007 (first entry)

XX

DE Mouse TM-1 (Tmem16a) protein.

XX

KW Cell isolation; stem cell; therapeutic; transgenic animal; screening;
KW tissue regeneration; genitourinary disease; uropathic;
KW intervertebral disk displacement; degeneration; injury; vulnerability;
KW back pain; transmembrane factor-1; Tmem16a.

XX

OS Mus musculus.

XX

PN WO2007027583-A2.

XX

PD 08-MAR-2007.

XX

PF 28-AUG-2006; 2006WO-US033491.

XX

PR 31-AUG-2005; 2005US-0713400P.

XX

PA (UYFL) UNIV FLORIDA RES FOUND INC.

XX

PI Harfe BD, Cohn MJ;

XX

DR WPI; 2007-412931/39.

DR N-PSDB; AFB77189.

XX

PT Isolating sonic hedgehog expressing-cells comprises obtaining a non-human
PT transgenic subject in which a marker gene has been inserted into the
PT subject's genome.

XX

PS Disclosure; SEQ ID NO 2; 96pp; English.

XX

CC The present invention relates to a method of isolating cells in selected
CC tissues co-expressing the sonic hedgehog (Shh) gene and a marker gene.
CC The method involves obtaining a non-human transgenic subject in which a
CC marker gene has been inserted into the subject's genome and isolating
CC Shh/marker gene expressing cells and Shh/marker gene non-expressing cells
CC from the selected tissue. The invention further provides a method of
CC identifying differentially expressed genes (e.g. transmembrane factors TM

CC -1 and TM-2, EST 1437418, Mmu-miR-135a-2 and AP-2 beta) in selected
CC tissues co-expressing the sonic hedgehog gene and a marker gene. The
CC invention is useful in tissue engineering, regeneration, reconstruction
CC and/or repair of tissues and genitourinary system and also in treating
CC intervertebral disk rupture, degeneration, disease or injury and back
CC pain. The invention is further useful for generating transgenic animal.
CC The present sequence is the mouse TM-1 (Tmem16a) protein.

xx

so Sequence 1017 AA:

Query Match 30.1%; Score 1489; DB 12; Length 1017;
Best Local Similarity 37.5%; Pred. No. 3e-143;
Matches 361; Conservative 170; Mismatches 303; Indels 128; Gaps 29;

Qy 26 GLYCRDQAHERWAMT--SETSSGHCARSRMLRRRAQEEDSTVLIDVSPPEAEKRGSGY 83
||| || : : : ||| ||| ||| : | : |:
Db 109 GLYFRDGKRVDYIILVYHHKRASG----SRTLARRGLONDML-----GTRS 151

Qy 84 STAHASEPGQQAACRAGSPAKPRIADFVLVWEEDLKLDRQDSAARDRTDMHRTWRET 143
|| : : |||| | :| :| | ||
Db 152 VRODOPPLPG--KGSPVDAKSPEVP-----MDYHEDD-----KFRRREE 187

Qy 201 NWSAGLLAWLGIPNVLLEVVVPDPVPEYYSCRFRVNKLPRFLGS-----DNQDTFFT 251
 : ||| | : | :: : | : | | : | : | : | : | : |||
Db 244 --TRGLLK--TINSVLOKITDPIOPKVAEHRPOTTKRLSYPSREKOHLFEDLTDRDSEED 299

Qy 252 STKRHQILFEILAKTPYGHKEKKNLGLIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLN 311
| | | :||| : | | : | ||| | | :| | | : | | | |
Db 300 SKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYSAAYPLHDGDPY---EGDNV-REFN 353

Qy 312 QRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLPAAVGTLVFLVG 371
|:|:|:| | :|:|:| |:|:|:|:| |:|:|:|:| |:|:|:|:| |:|:|:|:| |:|:|:|
Dy 354 DRKLLYEEWASYGVYKYQPTDILVRKYFGEKVGLYFAWLGAYTOMLTPASIVGVIVFLYG 413

Qy 431 ALWAVLLEWKRKSATLAYRWDCSDYEDTEE---RPRPQFAA----SAPMTAPNPIT 481
||| :|:||| | ||| : :|: || | || :: | | | : | |
Dy 474 ALWAATEMEHWKPKOMPLNYPWDLTGEEEEEFAVKDHPRAEYARVLEKSLRKESPRNKET 533

Qy 482 GEDEPYFPERSRARMLAGSVVIVVMVVVCLVSIILYRAIMAIIVSRSRGNTLLAAWA 541
|: | | |: |:|| :: :|:|| | :: : : : :
Dy 534 --DKVKLTWPRDPRAYETNIVSLEMIAVTEALVIGVLTVDISTAAANAMNSSPSVRNT 591

Qy 542 SRIASLTGSVNVLFILILSKIYVSLAHVLRWEMHRTQTKFEDAFTLKVFIFQFVNFSY 601
 : | ::||| ::| ::| : ||: | : ::| ||: | | | : ||| :|
 Db 592 RVTVTATAVIINLVVIILDEVYGCIAIRWLTKIEVPKTEKSFEERLTFKAFLLKVFVNSYT 651

Qy 602 SPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQE 659
 |:||||| | :| :| | | | | | :| :| :| :| :| :|
 Db 652 PIFYVAFFKGRFVGPRGDYVYIFRSFRMEECAPGGCLMELCIQLSIIIMLGKQLIQNNLFE 711

Qy 660 VLIPKLKGWWQKFRLRSKKRAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVT 719
 : | ||:| : : :|| : : :| | : | | | | | | :| :| :|
 Db 712 IGIPKMKKFIRYKLRLRQSPSDREEVYVKRKQRYEVDFNLEPFAGLTPEYMEMIIQFGFVT 771

Qy 720 IFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIFHILAGLTHLAVIS 779
 :|||: | | | | | :| | | | | | | | | | | | | | | | |
 Db 772 LFVASFPLAPLFALLNNIIEIRLDAKKFVTELRRPVAIRAKDIGIWINILRGVGKLA VII 831

Qy 780 NAFLLAFASSDFLPRAYYRWTRAHD--LRGFLNFTLARAPSSF-----AAAHN----- 824
 | |:::| :| | :| | : : :| :| | | | | | | | | | | |
 Db 832 NAFVISFTSDFIPRLVYLYMYSQNGTMHGFBVNHTL---SSFNVSDFQNGTAPNDPLDG 887

Qy 825 ---RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVFSVGRLLDLPDIP 876
 : | |: | :| :| | | | | | | | | | | | | | | | | | |
 Db 888 YEVOQICRYKDYREPPWSEHKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIP 947

Qy 877 ESVEIKVKREYYL-----AKQALAEENEVLFGTNGTKDEQPKGSELSSSHWTPTFV 926
 : : | :| | | | | | | | | | | | | | | | | | | | | |
 Db 948 KDISQQIHKEKVLMLVELMFREEQGKQQLLDTWM-----EKEKPRDVPCNNH-SPTTHP 999

Qy 927 KA 928
 :|
 Db 1000 EA 1001

RESULT 11

AEG11142

ID AEG11142 standard; protein; 960 AA.

XX

AC AEG11142;

XX

DT 15-JUN-2007 (revised)

DT 20-APR-2006 (first entry)

XX

DE Human transmembrane protein 16A, SEQ ID NO: 7.

XX

KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;

KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;

KW transmembrane protein 16A;

KW transmembrane protein 16A (eight membrane-spanning domains);

KW oral cancer overexpressed 2; membrane protein;
KW tumor amplified and overexpressed sequence 2;
KW transmembrane protein 16A [Homo sapiens]; TMEM16A; TAOS2; ORAOV2;
KW FLJ10261.
XX
OS Homo sapiens.
XX
PN US2006040292-A1.
XX
PD 23-FEB-2006.
XX
PF 08-JUL-2005; 2005US-00177894.
XX
PR 08-JUL-2004; 2004US-0586676P.
XX
PA (WEST/) WEST R B.
PA (VRIJ/) VAN DE RIJN M.
XX
PI West RB, Van De Rijn M;
XX
DR WPI; 2006-182760/19.
DR N-PSDB; AEG11136.
DR REFSEQ; NP_060513.
DR PC:NCBI; gi40354210.
XX
PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT positive subclass, involves detecting expression or activity of gene
PT encoding DOG1 polypeptide in sample.
XX
PS Disclosure; SEQ ID NO 7; 177pp; English.
XX
CC The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predictive information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by
CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 960 AA;

Query Match 30.1%; Score 1488; DB 11; Length 960;
 Best Local Similarity 37.6%; Pred. No. 3.5e-143;
 Matches 363; Conservative 160; Mismatches 307; Indels 136; Gaps 28;

Qy 26 GLYCRDQAHAEWAMT--SETSSGSHCARSRMLRRRAQEEEDSTVLIDVSPPEAEKRGSYG 83
 |||| || :: : || : || || || |:
 Db 52 GLYFRDGRRKVVDYILVYHHKRPSG----NRTLVRVQHSDTP-----SGA 92

Qy 84 STAHASEPQQQAAACRAGSPAKPRIADFVLVWEEDLKLDRQDQAARDRTDMHRTWRET 143
 : | : | : || | : | : | | : | || | | : | || | | : |
 Db 93 RSVKQDHPLPGKGASLDAGSGEPP-----MDYHEDD-----KFRREE 130

Qy 144 FLNDNLRAAGLCVDQQDVGQDNTTVH---YALLSASAWVLCYAAEDLRLKLPLQELPNQAS 200
 : || || || :: : | : | : | : : | | || | | : || | : | : |
 Db 131 YEGNLLEAGLELE---RDEDTKIHGVGFVKIHAPWNVLCREAELFLKLKMPKKMYH--I 184

Qy 201 NWSAGLLAWLGIPNVLLEVVPDVPEYYSCR-----FRVNKLPLRFLGSDNQDTFF 250
 | : || | | : || : | : | | | | | | | | | | : | : |
 Db 185 NETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYPFSREKQHFLDLSD-KDSFF 241

Qy 251 TSTKRHQILFEILAKTPYGHKEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRL 310
 | | | : || | : | | : | : | | | | | | | | | : | : |
 Db 242 DSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHDGDY----NGENVEF 295

Qy 311 NQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTFLVFLV 370
 | | : | : | | : | | : | : | : | : | | | | | | | : | : |
 Db 296 NDRKLLYEEWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIIVFLY 355

Qy 371 GCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLSSACALAQAGRLFDHGGTVFFSLF 429
 | | : | : | : | : | | | | | | | | | | | | | | | | | : |
 Db 356 GCATMDENIPSMEMCDQRHNITMCPCLCDKTCSYWKMSACATARASHLFDNPATVFFSVF 415

Qy 430 MALWAVLLEYWKRKSATLAYRWDCTSDEYDTEE---RPRPQFAA----SAPMTAPNPI 480
 | | | | : | : | | | | : | | | | | | | | | | | | | | | |
 Db 416 MALWAATFMEHWKRQKQMRNLNYRWDLTGFEEEEEAVKDHPRAEYEARVLEKSLKKESRNKE 475

Qy 481 TGEDEPYFFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNLILLA 540
 | | : | | | | | | : | : | | : | : | | | | | | | | | | |
 Db 476 T--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRN 533

Qy 541 ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTREWMHRTQTKFEDATLKVIFQFVNFY 600
 | | : | : | : | : | | | | | | | | | | | | | | | | | | |
 Db 534 IRVTVTATAVIINLVVIIILLDEVYGCiarwlktievpkteksfeerlifkafllkfvnsy 593

Qy 601 SSPVYIAFFKGRFVGPGNYHTLF--GVRNEECAAGGCLIELAQELLVIMVGKQVI--NNMQ 658
 | | : | : | : | : | | | | | | | | | | | | | | | | | | |
 Db 594 TPIFYVAFFKGRFVGPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLF 653

Qy 659 EVLIPKLKGWWQKFLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFV 718

Db	654	EIGIPKMKKLIRYLKLKQQSPPDHEECVKRKQRYEVVDYNLEPFAGLTPEYMEMIIQFGFV	713
Qy	719	TIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGHFILAGLTHLAVI	778
Db	714	TLFVASFPLAPLFAALLNNIIEIRLDAKKFVTELRRPVAVRAKDIGIWINILRGIGKLAVI	773
Qy	779	SNAFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN-----	824
Db	774	INAFVISFTSDFIPRLVYLYMYSKNGTMHGFVNHTL---SSFNVSDFQNGTAPNDPLDL	829
Qy	825	---RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLVPDI	875
Db	830	GYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVWDVIPDI	889
Qy	876	PESVEIKVKREYYLA-----KQALAEENEVLFGTNGTKDEQP-----KG	913
Db	890	PKDISQQIHKEVKVLMVELFMREEQDKQQLL--ETWMEKERQKDEPPCNCNHTKACPDSL	947
Qy	914	SELSSH	919
Db	948	SPAPSH	953

RESULT 12

AEG11146

ID AEG11146 standard; protein; 840 AA.

XX

AC AEG11146;

XX

DT 15-JUN-2007 (revised)

DT 20-APR-2006 (first entry)

XX

DE Human transmembrane protein 16A, SEQ ID NO: 11.

XX

KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;
KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;
KW TMEM16A protein; TMEM16A protein [Homo sapiens].

XX

OS Homo sapiens.

XX

PN US2006040292-A1.

XX

PD 23-FEB-2006.

XX

PF 08-JUL-2005; 2005US-00177894.

XX

PR 08-JUL-2004; 2004US-0586676P.

XX

PA (WEST/) WEST R B.
PA (VRIJ/) VAN DE RIJN M.
XX
PI West BB. Van De Rijn M.

DB WBT: 2006-182760/19

DB N=PSDB: AEG11141

DR GENBANK: AAH33036

DB PC:NCBI: gi34192278

xx

PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT positive subclass, involves detecting expression or activity of gene
PT encoding DOG1 polypeptide in sample.

XX

PS Disclosure; SEQ ID NO 11; 177pp; English.

XX

CC The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTS) and tumors other than GISTS.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predictive information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by
CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.

CC

CC Revised record issued

CC information from BON

XX

Sequence 840 AA;

Query Match 29.9%; Score 1479.5; DB 11; Length 840;
Best Local Similarity 40.0%; Pred. No. 2.2e-142;
Matches 340; Conservative 152; Mismatches 270; Indels 89; Gaps 22;

6 DDKFRRREEYEGNLLEAGLELE---RDEDTRIHGVGFVKIHAPWNVLCREAEFLKLKMP 61

Db 62 TKKMYH--INETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYPFSREKQHLFD 117

Qy 242 GSDNQDTFFTSTKRHQILFEILAKTPYGH EKKNLLGIHQLLAEGVLSAAFPLHDGPFKTP 301
|| :|:|| | | | :|| | :| :|| | ||| | :||:|||| :|

Qy 302 PEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLPA 361
 : | ::|::| |||:| : | |||:| |||:| |||:| |||:| |||:| |||:
 Db 173 --NGENVEFNDRKLLYEEWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPAS 230

Qy 362 VVGTIVFLVGCFLVFSIPTQELCGSKDSFEMCPLC-LDCPFWLSSACALAQAGRLFDH 420
 :||| :||| ||| : :|||: ||| : : |||:||| | :||| :||| :||| :|||:
 Db 231 IVGIIVFLYGCATMDENIPSMEMCDQRHNTMCPLCDKTCSYWMSSACATARASHLFDN 290

Qy 421 GGTVFFSLFMALWAVLLEYWKRKSATLAYERWDSCSDYEDTEERPRPQFAA----SAPMT 475
 |||||:||||| :|||:||| | ||| :||| :||| :||| :||| :|||:
 Db 291 PATVFFSVMALWAATFMEHWKRKQMRNLNRYRDLTGFEEDHPRAEYEARVLEKSLKKE 350

Qy 476 APNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAIIVVSRSNT 535
 :| | | |: | | | | | |: | :||| :||| :||| :||| :||| :|||:
 Db 351 SRNKET--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIYRISMAALAMNSP 408

Qy 536 LLAAWASRIASLTGSVVNLVFILELILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQ 595
 : : : | :||| |::| :||| :||| :||| :||| :||| :||| :|||:
 Db 409 SVRSNIRVTVTATAVIIINLVVIIILLDEVYGCIAWRLTKEVPKTEKSFEERLIFKAFLK 468

Qy 596 FVNFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQUELLVIMVGKQVI 654
 ||| |: | :||||| |||: | : | | | | |||:||| :| :|||:|||:
 Db 469 FVNSYTPIFYVAFFKGRFVGPRGDYVYIIFRSFRMEECAPGGCLMELCIQLSIIIMLGKQLI 528

Qy 655 -NNMQUEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCCEGLFDEYLEMVL 713
 |||: |: | |||: | : | :| : | : | | | | |||:|||:
 Db 529 QNNLFEIGIPKMKKLIRYLLKQQSPPDHEECVKRKQRYEVNDYNEFAGLTPEYMEMII 588

Qy 714 QFGFVTIFVAACPLAPLFALLNNWEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLT 773
 |||||:|||: | | |||:|||: | :|||:||| | | |||:|||:|||:
 Db 589 QFGFVTIFVASFPLAPLFALLNNIEIRLDAKKFVTELRRPVAVRAKDIGIWYNILRGIG 648

Qy 774 HLAVISNAFLAFLSSDFLPR--YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN 824
 |||| :|||:|:|||:||| | :||| :|||:||| ||| | | | | | | |
 Db 649 KLAVIDAFVISFTSDIFIPRLVYLYMYSKNGTMHGFVNHTL---SSFNVSDFQNGTAPN 704

Qy 825 -----RTCRYRAFRD--DDGHY--SQTYWNLLAIRLAFVIVFEHVVFSVGRLLDL 870
 :|||: |:| :| :| | :| :||| | |||:|||:|||:||| :| :|
 Db 705 DPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLARLAFVIVFQNLVMFMDSFVDW 764

Qy 871 LVPDIPESVEIKVKREYYLA-----KQALAEENEVLFGTNGTKDEQP----- 911
 :|||: |:| :| | | | | | | | | | | | | | | | | | | |
 Db 765 VIPDIPKDISQOIHKEVKLVMVELMREEQDKQQLL--ETCMEEKERQKDEPPCNHHNTKAC 822

Qy 912 ---KGSELSSH 919
 ||| |||
 Db 823 PDSLGPAPSH 833

RESULT 13
ADG48280
ID ADG48280 standard; protein; 1003 AA.
XX
AC ADG48280;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human retina-specific protein - C12orf3variants.
XX
KW human; retina-specific protein; NETO1; retinal disease;
KW age related macular degeneration; night blindness; C12orf3variants.
XX
OS Homo sapiens.
XX
PN WO2003068967-A2.
XX
PD 21-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001625.
XX
PR 18-FEB-2002; 2002EP-00003675.
PR 21-FEB-2002; 2002US-0357857P.
XX
PA (LYNK-) LYNKEUS BIO TECH GMBH.
XX
PI Stoehr BH, Weber FHB, Goehring F;
XX
DR WPI; 2003-767334/72.
DR N-PSDB; ADG48279.
XX
PT New nucleic acid encoding retinal protein sNETO1, useful for diagnosis of
PT retinal disease, especially macular degeneration, also for drug screening
PT and therapy.
XX
PS Claim 18; Fig 14; 199pp; English.
XX
CC The invention comprises the amino acid and coding sequences of a human
CC retina-specific protein - NETO1. The DNA and protein sequences of the
CC invention are useful in the treatment of retinal diseases, such as
CC macular degeneration (especially age related) and night blindness. The
CC present amino acid sequence represents the human retina-specific protein
CC C12orf3variants.
XX
SQ Sequence 1003 AA;

Query Match 29.6%; Score 1464; DB 7; Length 1003;
Best Local Similarity 37.4%; Pred. No. 1.1e-140;

Qy 758 RAQDIGIWPHILAGLTHAVISNAFLAFLPRAYYRWTRAHD--LRGFLNFTLA-- 813
 | :||||||| ||:|: :|||||||::| :|||:||| |::: :|: | ||:| ||:
 Db 796 RTKDIGHWFDILSGIGKFSVISNAFVIAITSDFIPRLVYQYSYSHNGTLHGFVNHTLSFF 855

Qy 814 -----RAPSSFAAAHNRTCRYRAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEH 859
 : :| : : ||:: :|: : :|| | :|: |||||:||:
 Db 856 NVSQLKEGTQPNPENSQFDQEVQFCRFKDYREPPWAPNPYEF SKQYWFILSARLAFVIIIFQN 915

Qy 860 VVFSVGRLLDLPDIPESVEIKVKRE-----YYLAKQALAEANEVLFGTNGTKDEQPKG 913
 :| : |:| :||| | : :||:| :|| : |:| | : | | |:
 Db 916 LVMFLSVLVDWMIPDIPDISDQIKKEKSSLVDFFLKE---EHEKLKLMDEPALRSPGG 971

Qy 914 SELSSHWTPTVPKA-SQL 931
 : | : | |||:
 Db 972 GDRSRSRASSAPSGQSQL 990

RESULT 14

AEH82071

ID AEH82071 standard; protein; 913 AA.

XX

AC AEH82071;

XX

DT 15-JUN-2007 (revised)

DT 13-JUL-2006 (first entry)

XX

DE Human gnathodiaphyseal dysplasia protein, GDD1.

XX

KW Osteopathic; Gene therapy; bone disease; bone injury; bone resorption;
 KW gnathodiaphyseal dysplasia; GDD1; BOND_PC; transmembrane protein 16E;
 KW integral membrane protein GDD1; transmembrane protein 16E [Homo sapiens];
 KW TMEM16E; GDD1; integral membrane protein GDD1 [Homo sapiens]; GO5783;
 KW GO16020; GO16021.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Inhibitory-site 356

FT /note= "Missense mutations in the coding sequence can
 FT lead to substitution of this residue with either Arg or
 FT Gly"

XX

PN JP2006121961-A.

XX

PD 18-MAY-2006.

XX

PF 28-OCT-2004; 2004JP-00313511.

XX

PR 28-OCT-2004; 2004JP-00313511.

XX

PA (UYTO-) UNIV TOKUSHIMA NAT UNIV CORP.

XX

PI Itakura M, Tsutsumi S, Kamata N, Inoue H;

XX

DR WPI; 2006-367194/38.

DR N-PSDB; AEH82070.

DR PC:NCBI; gi47106048.

DR PC:SWISSPROT; Q75V66.

XX

PT Novel gnathodiaphseal dysplasia DNA, useful as diagnostic agent for bone

PT disease such as gnathodiaphseal dysplasia, bone deficiency or bone-

PT resorption property disease.

XX

PS Claim 9; SEQ ID NO 2; 11pp; Japanese.

XX

CC The present invention relates to a human gnathodiaphyseal dysplasia (GDD) coding sequence (GDD1; AEH82070) and encoded protein (AEH82071). GDD1 is useful as a bone disease diagnostic agent, where the bone disease is GDD, bone deficiency and/or bone-resorption property disease, where the GDD disease causes hardening of bone, susceptibility to fracture, cement bone pathology of a lower jaw bone, etc. GDD1 is also useful in bone formation regeneration, hard tissue reconstruction, etc., and in research application.

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed information from BOND.

XX

SQ Sequence 913 AA;

Query Match 29.4%; Score 1455; DB 11; Length 913;
 Best Local Similarity 38.6%; Pred. No. 8.4e-140;
 Matches 325; Conservative 154; Mismatches 276; Indels 86; Gaps 22;

Qy 108 RIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLNRAAGL---CVDQQDVQDGN 164
 | |||| : ::|| | :: | ||| || |::| :||

Db 78 RQIDFVLSYVDDVKKD-----AELKAERRKFETNLRKGTGLELEIEDKRDSEDGR 127

Qy 165 TTVHYALLSASAWAVLCYYAEDLRLKLPLQE--LPNQASNWSAGLLAWLGINPVNLLEVVPD 222
 | :: : | || | || | :||:||:| :| :| :| :| | |

Db 128 T-YFVKIHAPWEVLVTYAEVLGIKMPIKESDIPRPKHTPISYVLGPVRLP--LSVKYPH 183

Qy 223 VPPEYYSCRFRVNKLPRFLGSDNQDFTFTSTKRHQILFEILAKTPYGHKEK-KNLLGIHQL 281
 ||||: :| :: || | | || | :| :||:||:| :| | | | :|

Db 184 --PEYFTAQFSRHRQELFLIED-QATFFPSSSRNIRVYYILSRCFGIEDGKKRFGIERL 240

Qy 282 LAEGVLSSAFAFLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWKGKWNKYQPLDHVRYYFGE 341
 | |:::||| : | | | |:| | |:||: | | ||| : | | ||| :| :|||

Db	241 LNSNTYSSAYPLHDGQYWKPSEPPNP--TNERYTLHQNWARFSYFYKEQPLDLIKNYGE	298
Qy	342 KVALYFAWLGFYTGWLLPAAVVGTFLVFLVGCFLVFSIDIPTQELCGSK--DSFEMCPLCLD	399
Db	299 KIGIYFVFLGFYTEMFFAAVVGACFIYGLLSMEHNTSSTEICDPEIGGQMIMCPLCDQ	358
Qy	400 -CPFWLSSACALAQAGRLFDHGGTVFFSLFMAILWAVLLEWKRKSATLAYERWDCSDYE	458
Db	359 VCDYWRNLNSTCLASKFSHLDNESTVFFAIFMGIWVTLFLEFWKQRQARLEYEWDLVDFE	418
Qy	459 DTEE--RPRPQFAASAPMTAPNPITGEDEPYFPERSRARMLAGSVVIVVMVAVVMCLV	516
Db	419 EEEQQQLQLRPEFEAMCKHRKLNNAVTKEMEPYMPYTRIPWYFLSGATVTLWMSLWVTSMV	478
Qy	517 SIILYRAIMAIIVVSRSGNTLLAAWASRI-----ASLTGSVVNLVFIL	558
Db	479 AVIVYRL-----SVFATFASFMESDASLKQVKSFLTPQITTSLTGSCLNFIVIL	527
Qy	559 ILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPG	618
Db	528 ILNFFYKEKISAWITKMEIPRTYQEYESSLTLKMFQFVNFYSSCFYVAFFKGKFGVGYPG	587
Qy	619 NYHTLFGV-RNEECAAGGCLIELAQELLVIMVGKQVINNMQEVILPKLKQWWQKFRLRSK	677
Db	588 KYTYLFNEWRSEECDPGGCLIELTTQLTIIMTQKQIFGNIKEAIYPLALNWW-----R	640
Qy	678 KRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLFALLN	735
Db	641 RRKARTNSEKLYSRWEQDHLESFGPLGLFYEYLETVTQFGFVTFLVASFPLAPLLALIN	700
Qy	736 NWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFLSSDFLPRAY	795
Db	701 NIVEIRVDAWKLTQYRRTVASKAHSIGVWQDILYGMALSVATNAFIVAFTSDDIIPRLV	760
Qy	796 YRW---TRAHDLRGFLN----FTLARAPSSFAAAHN--TCRYRAFR---DDDGHY-	839
Db	761 YYYAYSTNATQPMTGYVNNSLSVFLIADFPNHTAPSEKRDFFTCRYRDYRYPDDENKYF	820
Qy	840 -SQTWNLLAIRLAFVIVFEHVVFSVGRLLDLPDIPIESVEIKVKREYYLAKQALAEENE	898
Db	821 HNMQFWHVLAAKMTFIIVMEHVVFLVKFLAWMIPDVKDVVERIKREKLMTIKILHDFE	880
Qy	899 V 899	
Db	881 L 881	

RESULT 15
ABB62812

ID ABB62812 standard; protein; 1219 AA.
XX
AC ABB62812;
XX
DT 15-JUN-2007 (revised)
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 15228.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; BOND_PC; CG6938-PA; CG6938-PA [Drosophila melanogaster];
KW CG6938.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL06915.
DR PC:NCBI; gi24663059.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 15228; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp://ftp.wipo.int/pub/published_pct_sequences

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 1219 AA;

Query Match 29.2%; Score 1445; DB 4; Length 1219;
Best Local Similarity 35.6%; Pred. No. 1.4e-138;
Matches 342; Conservative 165; Mismatches 332; Indels 122; Gaps 27;

Qy 35 AERWAMTSETSSGSHCARSRML-----RRRAQEEDSTVLIDVSPPEAEKRGSY 82
| : | : | || | : | : | : | : | : | : |
Db 249 ADRVNQSYESVMESSH---SNVLPDQFQGYRQLIPTERKASDTASSV-----SGSY 294

Qy 83 GSTAHASEP---GGQQAACRAGSPAkp-----RIADFVLVW-EEDLKLDRQ 125
: | : | | : | : | : | : | | | | | : | : |
Db 295 YGSRKASKSNLGGESGDERRVSKQDREGLDPESLMFRDGRKVDMVLAWEEDLGMTE 354

Qy 126 QDSAARDRTDMHRTWRETFLDNLRAAGLCLVCDQQD-VQDGNTTVHYALLSASAWVLCYAAE 184
: | | | | : | : | : | | | | | | : | : | : |
Db 355 AEAKRRDN-----RRSFMENLIKEGLEVELEDKSQSNEKTFKLKIHLPWRLETRLAE 407

Qy 185 DLRLKLP-----LQELPNQASNWSAGLLAWLGLIPNVLLEVVPDVPP 225
: | | | | : | : | | | : | : | : | : |
Db 408 VMNLKLPVKRFITISVKPSWDEENVVLRNMQYWKDVWQR-LTKKIQLDQTLLE---GET 462

Qy 226 EYYSRFRVNKLPRFLGSDNQDFTTSTKRHQILFEILAKTPYGHKEKKNLLGIHQLLAEG 285
: | | : | : | : | | | : | : | : | : | : |
Db 463 TPKAATANGNPEEQFIVKD-RATAFTAQSRLSMLVMQVLIRTPFDESDRS--GIRRLMNDG 519

Qy 286 VLSAAFPLHDGPFKTPPEGPQAPRLN-QRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVA 344
| | | : | : | : | : | : | : | : | : | : |
Db 520 TYLGCFCPLHEGRY---DRPHSSGISLDRRVLYQTWAHPSQWYKKQPLCLVRKYFGDKIA 575

Qy 345 LYFAWLGFYTGWLLPAAVGVTLFLVGFCLFLVSD--IPTQELCG--SKDSFEMCPLC-LD 399
| | | | | | | : | | | | | : | : | : | : |
Db 576 LYFCWLGFYTEMVLPAPAVGTLCFIYGLATLESEDNTPSKEICNEYGTGNITLCPLCDKA 635

Qy 400 CPFWLLSSACALAQAGRFLDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYED 459
| : | | : | : | : | : | : | : | : | : |
Db 636 CSYQRLESSESCLFSRRLTYLFDNPSTVFFAIFMSFWATTFLELWKRKQSVLWWEVDLHNV-D 694

Qy 460 TEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARMLAGSVVIVVMVAVVVMCLVSI 519
: | | | : | : | | | : | : | : | : | : |
Db 695 MDEENRPEFETNATTFRMNPVTREKEPYMSTWNRSIRFVITGSAVLFMISVVLSAVLGTTI 754

Qy 520 LYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNLVFILILSKIYVSLAHVLTRWEMHRT 579
| | : | : | : | : | : | : | : | : | : |
Db 755 LYRITLVSIVYGGGGFFVKEHAKLFTSVTAALINLVVIMILTRIYHRMMAIKLTNLENPRT 814

Search completed: June 24, 2008, 08:45:38
Job time : 270 secs